**AMENDMENTS TO THE CLAIMS** 

This listing of claims will replace all prior versions and listings of claims in the

application:

**LISTING OF CLAIMS:** 

1. (currently amended): A method for the detection of a base sequence of interest in a

sample polynucleotide consisting essentially of the steps of:

(1) contacting the sample polynucleotide with at least one kind of probe polynucleotides

in an aqueous solution to form a hybridization complex;

(2) isolating the hybridization complex;

(3) dissociating the hybridization complex to recover the probe polynucleotides; and

(4) identifying the probe polynucleotides to detect the base sequence of interest in the

sample polynucleotide;

wherein each base sequence of interest in the sample polynucleotide is identified by one

probe complementary to the base sequence of interest.

2. (previously presented): The method according to claim 1, wherein the hybridization

is carried out in such a manner that none of the sample polynucleotide or the probe

polynucleotides are immobilized.

**3.** (previously presented): The method according to claim 1 or 2, wherein plural kinds

of probe polynucleotides are used to detect plural base sequences of interest.

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**4.** (previously presented): The method according to claim 1 or 2, wherein the probe

polynucleotides are labeled with fluorescent substance.

**5.** (previously presented): The method according to claim 1 or 2, wherein the probe

polynucleotides are identified by means of hybridization with a polynucleotide chain

complementary thereto.

**6.** (previously presented): The method according to claim 5, wherein the

polynucleotide chains complementary to the probe polynucleotides are immobilized.

7. (previously presented): The method according to claim 6, wherein the immobilized

polynucleotide chain complementary to the probe polynucleotides are in the form of a DNA or

RNA chip.

**8.** (previously presented): The method according to claim 1 or 2, wherein plural kinds

of probe polynucleotides are used to detect plural, non-contiguous base sequences of interest.

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